

APPLICANT: John Greene and Craig A. Rosen
TITLE OF INVENTION: Fibroblast Growth Factor-15
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
ADDRESSEE: CECCHI, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,169B
FILING DATE: 05 JUN 95
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33,073
REFERENCE/DOCKET NUMBER: 325800-441 (PF203)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 208 AMINO ACIDS
TYPE: AMINO ACID
STRANDEDNESS:
TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN
US-08-462-169B-20

Query Match 100.0%; Score 770; DB 1; Length 208;
Best Local Similarity 100.0%; Pred. No. 4e-78;
Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RHVRSYNHLOGDVRWRKLFSTFKYFLKIEKNGKVGSGTKKENCPSYLSILEITSVGIVAVK 60
DB 65 RHVRSYNHLOGDVRWRKLFSTFKYFLKIEKNGKVGSGTKKENCPSYLSILEITSVGIVAVK 124
QY 61 AINSNYLAMNKKGLYSGKEFNNDCKLKERIEBNGYNTYASFVWQHNGROMYVALNGKG 120
DB 125 AINSNYLAMNKKGLYSGKEFNNDCKLKERIEBNGYNTYASFVWQHNGROMYVALNGKG 184
QY 121 APRRGQKTRRKNNTSAHFLPMVVS 144
DB 185 APRRGQKTRRKNNTSAHFLPMVVS 208

RESULT 33
US-08-951-822-30
Sequence 30, Application US/08951822A
Patent No. 598966
GENERAL INFORMATION:
APPLICANT: Deisher, Theresa A.
APPLICANT: Conklin, Darrell C.
APPLICANT: Raymond, Fenella
APPLICANT: Bukowski, Thomas R.
APPLICANT: Holderman, Susan D.
APPLICANT: Hansen, Birgit
APPLICANT: Sheppard, Paul O.
TITLE OF INVENTION: NOVEL FGF HOMOLOGS
FILE REFERENCE: 96-20
CURRENT APPLICATION NUMBER: US/08/951,822A
CURRENT FILING DATE: 1997-10-16
NUMBER OF SEQ ID NOS: 36
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 30
LENGTH: 208

TYPE: PRT
ORGANISM: Homo sapiens
US-08-951-822-30
Query Match 100.0%; Score 770; DB 1; Length 208;
Best Local Similarity 100.0%; Pred. No. 4e-78;
Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RHVRSYNHLOGDVRWRKLFSTFKYFLKIEKNGKVGSGTKKENCPSYLSILEITSVGIVAVK 60
DB 65 RHVRSYNHLOGDVRWRKLFSTFKYFLKIEKNGKVGSGTKKENCPSYLSILEITSVGIVAVK 124
QY 61 AINSNYLAMNKKGLYSGKEFNNDCKLKERIEBNGYNTYASFVWQHNGROMYVALNGKG 120
DB 125 AINSNYLAMNKKGLYSGKEFNNDCKLKERIEBNGYNTYASFVWQHNGROMYVALNGKG 184
QY 121 APRRGQKTRRKNNTSAHFLPMVVS 144
DB 185 APRRGQKTRRKNNTSAHFLPMVVS 208

RESULT 34
US-09-103-079-20
Sequence 20, Application US/09103079A
Patent No. 6013477
GENERAL INFORMATION:
APPLICANT: Greene, John M.
APPLICANT: Rosen, Craig A.
TITLE OF INVENTION: Fibroblast Growth Factor 15
FILE REFERENCE: PF203D1
CURRENT APPLICATION NUMBER: US/09/103,079A
CURRENT FILING DATE: 1998-06-23
EARLIER APPLICATION NUMBER: 08/462,169
EARLIER FILING DATE: 1995-06-05
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 20
LENGTH: 208
TYPE: PRT
ORGANISM: Homo sapiens
US-09-103-079-20

Query Match 100.0%; Score 770; DB 2; Length 208;
Best Local Similarity 100.0%; Pred. No. 4e-78;
Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RHVRSYNHLOGDVRWRKLFSTFKYFLKIEKNGKVGSGTKKENCPSYLSILEITSVGIVAVK 60
DB 65 RHVRSYNHLOGDVRWRKLFSTFKYFLKIEKNGKVGSGTKKENCPSYLSILEITSVGIVAVK 124
QY 61 AINSNYLAMNKKGLYSGKEFNNDCKLKERIEBNGYNTYASFVWQHNGROMYVALNGKG 120
DB 125 AINSNYLAMNKKGLYSGKEFNNDCKLKERIEBNGYNTYASFVWQHNGROMYVALNGKG 184
QY 121 APRRGQKTRRKNNTSAHFLPMVVS 144
DB 185 APRRGQKTRRKNNTSAHFLPMVVS 208

RESULT 35
US-09-023-082A-2
Sequence 2, Application US/09023082A
Patent No. 607692
GENERAL INFORMATION:
APPLICANT: RUBEN, STEVEN M.
APPLICANT: JIMENEZ, PABLO
APPLICANT: DUAN, D. ROXANNE
APPLICANT: RAMPY, MARK A.
APPLICANT: MENDRICK, DONNA
APPLICANT: ZHANG, JUN
APPLICANT: NI, JIAN
APPLICANT: MOORE, PAUL A.
APPLICANT: COLEMAN, TIMOTHY A.

APPLICANT: GRUBER, JOACHIM R.
APPLICANT: DILLON, PATRICK J.
APPLICANT: GENTZ, REINER L.
TITLE OF INVENTION: KERATINOCYTE GROWTH FACTOR-2
NUMBER OF SEQUENCES: 148
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 NEW YORK AVE, NW, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,082A
FILING DATE: 13-FEB-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/01790
FILING DATE: 14-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/461,195
FILING DATE: 05-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/023,852
FILING DATE: 13-AUG-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/039,045
FILING DATE: 28-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/862,432
FILING DATE: 23-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/910,875
FILING DATE: 13-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/055,561
FILING DATE: 13-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: STEFFEE, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.0360008/EKS
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 208 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-023-082A-2

Query Match 100.0%; Score 770; DB 2; Length 208;
Best Local Similarity 100.0%; Pred. No. 4e-78;
Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	RHVSYNHLOGDVRWRKLFSTFYFLKIEKNKGVSGTKKENCPSYLEITSVIGVAVK	60
Db	65	RHVSYNHLOGDVRWRKLFSTFYFLKIEKNKGVSGTKKENCPSYLEITSVIGVAVK	124
QY	61	AINSNTYLANMKKGLYSGKEFNNDCKLKERIEENGNTYASFNWQHNGRQMTVALNGK	120
Db	125	AINSNTYLANMKKGLYSGKEFNNDCKLKERIEENGNTYASFNWQHNGRQMTVALNGK	184
QY	121	APRRGQTRRKNTSAHFLPMVHVS	144
Db	185	APRRGQTRRKNTSAHFLPMVHVS	208

RESULT 36
US-09-023-082A-20
Sequence 20, Application US/09023082A
Patent No. 6077692
GENERAL INFORMATION:
APPLICANT: RUBEN, STEVEN M.
APPLICANT: JIMENEZ, PABLO
APPLICANT: DUAN, D. ROXANNE
APPLICANT: RAMPEY, MARK A.
APPLICANT: MENDRICK, DONNA
APPLICANT: ZHANG, JUN
APPLICANT: NI, JIAN
APPLICANT: MOORE, PAUL A.
APPLICANT: COLEMAN, TIMOTHY A.
APPLICANT: GRUBER, JOACHIM R.
APPLICANT: DILLON, PATRICK J.
APPLICANT: GENTZ, REINER L.
TITLE OF INVENTION: KERATINOCYTE GROWTH FACTOR-2
NUMBER OF SEQUENCES: 148
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 NEW YORK AVE, NW, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,082A
FILING DATE: 13-FEB-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/01790
FILING DATE: 14-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/461,195
FILING DATE: 05-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/023,852
FILING DATE: 13-AUG-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/039,045
FILING DATE: 28-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/862,432
FILING DATE: 23-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/910,875
FILING DATE: 13-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/055,561
FILING DATE: 13-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: STEFFEE, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.0360008/EKS
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 208 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: protein
US-09-023-082A-20

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OM protein - protein search, using sw model

Run on: April 3, 2006, 05:33:45 ; Search time 12 Seconds
(without alignments)
365.303 Million cell updates/sec

Title: US-10-665-526-2_COPY_65_208
Perfect score: 770
Sequence: 1 RHVRSYNHLQGDVWRKLFSS.....GQTRKNTSAHFLPMVWHS 144

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 180808 seqs, 30441898 residues

Total number of hits satisfying chosen parameters: 180808

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA New.*
1: /SIDSS/ptodata/1/pubpaa/US08 NEW PUB.pep.*
2: /SIDSS/ptodata/1/pubpaa/US06 NEW PUB.pep.*
3: /SIDSS/ptodata/1/pubpaa/US07 NEW PUB.pep.*
4: /SIDSS/ptodata/1/pubpaa/PCT NEW PUB.pep.*
5: /SIDSS/ptodata/1/pubpaa/US09 NEW PUB.pep.*
6: /SIDSS/ptodata/1/pubpaa/US10 NEW PUB.pep.*
7: /SIDSS/ptodata/1/pubpaa/US11 NEW PUB.pep.*
8: /SIDSS/ptodata/1/pubpaa/US60 NEW PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	432.5	56.2	164	7	US-11-207-847-4
2	427	55.5	193	7	US-11-238-936-11
3	352.5	45.8	240	7	US-11-238-936-7
4	326	42.3	208	7	US-11-238-936-13
5	303	39.4	158	6	US-10-842-206-20
6	303	39.4	158	6	US-10-980-459-4
7	303	39.4	158	6	US-10-842-206-24
8	303	39.4	179	6	US-10-980-459-10
9	303	39.4	183	6	US-10-842-206-14
10	303	39.4	185	6	US-10-842-206-8
11	303	39.4	188	6	US-10-842-206-40
12	303	39.4	188	6	US-10-980-459-32
13	303	39.4	197	6	US-10-842-206-39
14	303	39.4	197	6	US-10-980-459-30
15	303	39.4	200	6	US-10-842-206-38
16	303	39.4	200	6	US-10-980-459-28
17	303	39.4	203	6	US-10-842-206-37
18	303	39.4	203	6	US-10-980-459-26
19	303	39.4	209	6	US-10-980-459-24
20	303	39.4	211	6	US-10-842-206-2
21	303	39.4	211	6	US-10-842-206-4
22	303	39.4	211	6	US-10-842-206-22
23	303	39.4	211	6	US-10-842-206-36
24	303	39.4	211	6	US-10-980-459-2
25	303	39.4	211	6	US-10-980-459-22

26	299	38.8	179	6	US-10-842-206-6
27	299	38.8	179	6	US-10-980-459-7
28	288	37.4	134	6	US-10-980-459-34
29	288	37.4	138	6	US-10-842-206-10
30	288	37.4	149	6	US-10-980-459-36
31	288	37.4	155	6	US-10-842-206-12
32	287	37.3	132	6	US-10-980-459-38
33	287	37.3	132	6	US-10-980-459-40
34	287	37.3	136	6	US-10-842-206-16
35	287	37.3	136	6	US-10-842-206-18
36	265.5	34.5	176	7	US-11-134-703-6
37	265.5	34.5	176	7	US-11-134-703-8
38	265.5	34.5	246	7	US-11-134-703-10
39	265.5	34.5	246	7	US-11-134-703-12
40	265.5	34.5	266	7	US-11-238-936-9
41	265.5	34.5	266	7	US-11-238-936-15
42	265.5	34.5	268	7	US-11-134-703-4
43	265.5	34.5	268	7	US-11-134-703-18
44	247	32.1	245	6	US-10-131-826A-280
45	247	32.1	245	6	US-10-973-115B-280

ALIGNMENTS

RESULT 1
US-11-207-847-4
; Sequence 4, Application US/11207847
; Publication No. US20060039892A1
; GENERAL INFORMATION:
; APPLICANT: DDE, Kimberly
; APPLICANT: LEE, Judithann
; TITLE OF INVENTION: METHODS OF HEALING WOUNDS BY
; TITLE OF INVENTION: ADMINISTERING HUMAN IL-18
; FILE REFERENCE: PU60998
; CURRENT APPLICATION NUMBER: US/11/207,847
; PRIOR FILING DATE: 2005-08-19
; PRIOR APPLICATION NUMBER: 60/603,012
; PRIOR FILING DATE: 2004-08-20
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 164
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-207-847-4

Query Match	56.2%	Score 432.5	DB 7	Length 164
Best Local Similarity	54.5%	Pred. No. 9.3e-37		
Matches	78	Conservative	30	Mismatches 34; Indels 1; Gaps 1
QY	1	RHVSYNHLQ-GDVRWRKLFSTFKYFLKIEKNGKVGSKENCPYSILEITSVEIGVAV	59	
Db	21	RHTRSYDMEGGDIRVRLFCRTQWYLRIDKRGKVGQEMKNYINMEIRTVAGIVAI	80	
QY	60	KAINSYNYLMMKKGKLYGSKFNNCKLKERTEENGYNITYASFNQHNGROMYVALNGK	119	
Db	81	KGVESEFYLAMNKEGKLYAKCEKNCNFKELILENHNTYASAKWTHNGEMFVALNQK	140	
QY	120	GAPRGQKTRRKNTSAHFLPMV 142		
Db	141	GIPVRGKTKKSKTAHFLPMAI 163		

RESULT 2
US-11-238-936-11
; Sequence 11, Application US/11238936
; Publication No. US20060025343A1
; GENERAL INFORMATION:
; APPLICANT: Whitehouse, Martha J.
; APPLICANT: Kavanaugh, Michael W.
; TITLE OF INVENTION: Angiogenically Effective Unit Dose of FGF and Method of
; TITLE OF INVENTION: Administering

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 3, 2006, 05:33:02 ; Search time 24 Seconds
(without alignments)
577.301 Million cell updates/sec

Title: US-10-665-526-2_COPY_65_208

Perfect score: 770

Sequence: 1 RHVRSYNHLQGVWRKLFSS.....GQTKRKNTSAHFLPMVVS 144

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 80:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	434.5	56.4	194	2 S49501	keratinocyte growth
2	432.5	56.2	194	1 A36301	fibroblast growth
3	429.5	55.8	194	2 I48610	keratinocyte growth
4	425.5	55.3	194	2 S26049	fibroblast growth
5	369	47.9	256	2 JC4627	fibroblast growth
6	363	47.1	220	2 I50588	fibroblast growth
7	358	46.5	237	1 S39582	transforming prote
8	352.5	45.8	245	1 TVNST2	transforming prote
9	341.5	44.4	239	1 S04742	fibroblast growth
10	326	42.3	208	2 S66486	fibroblast growth
11	326	42.3	208	2 A48137	fibroblast growth
12	319	41.4	207	2 JC5941	fibroblast growth
13	315	40.9	207	2 JC5940	fibroblast growth
14	304	39.5	208	2 JC7082	fibroblast sonatot
15	303	39.4	211	2 JC7353	fibroblast growth
16	302	39.2	212	2 JC7511	fibroblast growth
17	301	39.1	97	2 B46289	keratinocyte growth
18	297	38.6	98	2 B46289	keratinocyte growth
19	269	34.9	96	2 D46289	fibroblast growth
20	265.5	34.5	267	1 TVRUP5	fibroblast growth
21	262.5	34.1	264	2 A36207	fibroblast growth
22	262.5	34.1	266	2 S68144	embryonic fibrobla
23	249.5	32.4	192	2 S54407	embryonic fibrobla
24	248.5	32.3	187	2 S23595	embryonic fibrobla
25	241.5	31.4	208	2 S14192	fibroblast growth
26	239.5	31.1	208	2 S20102	fibroblast growth
27	239	31.0	168	2 J50718	fibroblast growth
28	236.5	30.7	194	2 I50710	fibroblast growth
29	203	26.4	146	1 S00185	basic fibroblast g

30	203	26.4	154	2 C37360	basic fibroblast g
31	203	26.4	154	2 A31674	basic fibroblast g
32	203	26.4	157	1 GKBOB	basic fibroblast g
33	203	26.4	210	2 A32398	basic fibroblast g
34	202	26.2	155	1 A33665	acidic fibroblast
35	201	26.1	413	2 H88481	protein let-756 [l
36	200	26.0	155	2 D37360	acidic fibroblast
37	200	26.0	155	2 S04147	acidic fibroblast
38	198	25.7	155	1 A60721	acidic fibroblast
39	198	25.7	164	2 S31622	basic fibroblast g
40	197	25.6	155	1 GKBOA	acidic fibroblast
41	196	25.5	152	2 JH0476	acidic fibroblast
42	196	25.5	155	2 JH0055	acidic fibroblast
43	195.5	25.4	206	1 TVHUHS	fibroblast growth
44	195	25.3	189	2 A48834	basic fibroblast g
45	194	25.2	155	2 A60130	acidic fibroblast

ALIGNMENTS

RESULT 1

S49501

keratinocyte growth factor - sheep

C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004

C:Accession: S49501

R:Mitchell, J.E.A.; McInnes, C.J.

submitted to the EMBL Data Library, October 1994

A:Description: Cloning of a cDNA encoding ovine keratinocyte growth factor.

A:Reference number: S49501

A:Accession: S49501

A>Status: Preliminary

A:Molecule type: DNA

A:Residues: 1-194 <MIT>

A:Cross-references: UNIPROT:P48808; UNIPARC:UPI000012A719; EMBL:Z46236; NID:g559503; P1

C:Superfamily: fibroblast growth factor

Query Match 56.4%; Score 434.5; DB 2; Length 194;

Best Local Similarity 54.5%; Pred. No. 1.5e-33;

Matches 78; Conservative 30; Mismatches 34; Indels 1; Gaps 1;

QY	1	RHVSYNHLQ-GDVRWRKLFSTFKYFLKIKRNGKVGSTKKKNCPSILTSVEIGVAV 59
Db	51	RHRSYDYMEGDIRVRLFCRTQWLRIDKRGKVGKTQEMKNYINMEIRTVAVGIVAI 110
QY	60	KAINSYNYLANMKKGLYGSKEFNNDCKLKEIENGYNNTYASFVWQHNGRQMYVALNGK 119
Db	111	KGVESEYLANMKKGLYAKKECEDCNPKELILENHNTYASAKWTHSGGEMFVALNSK 170
QY	120	GAPREGQTKRKNTSAHFLPMVV 142
Db	171	GVFVRGKTKTKKQKTAHFLPMAI 193

RESULT 2

A36301

fibroblast growth factor 7 precursor [validated] - human

N:Alternate names: keratinocyte growth factor

C:Species: Homo sapiens (man)

C>Date: 28-Mar-1991 #sequence_revision 07-Jul-1995 #text_change 09-Jul-2004

C:Accession: A36301; A31453; A46289; I51958

R:Finch, P.W.; Rubin, J.S.; Miki, T.; Ron, D.; Aaronson, S.A.

Science 245, 752-755, 1989

A>Title: Human KGF is FGF-related with properties of a paracrine effector of epithelial

A:Reference number: A36301; MOID:89368897; PMID:2475908

A:Accession: A36301

A:Molecule type: mRNA

A:Residues: 1-194 <FIN>

A:Cross-references: UNIPROT:P21781; UNIPARC:UPI0000040660; GB:M60828; NID:g186738; P1D

R:Rubin, J.S.; Osada, H.; Finch, P.W.; Taylor, W.G.; Rudikoff, S.; Aaronson, S.A.

Proc. Natl. Acad. Sci. U.S.A. 86, 802-806, 1989

A>Title: Purification and characterization of a newly identified growth factor specific

GenCore version 5.1.7

Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 3, 2006, 05:31:58 ; Search time 230 Seconds

(without alignments)

441.722 Million cell updates/sec

Title: US-10-665-526-2_COPY_65_208

Perfect score: 770

Sequence: 1 RHVRSYNHLQGDVWRKLF.....GQTRKNTSAHFLPMVHS 144

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt_05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	770	100.0	170	2	Q8NF19 HUMAN
2	770	100.0	208	1	Q8NF19 HUMAN
3	770	100.0	208	2	Q8NF19 HUMAN
4	770	100.0	208	2	Q8NF19 HUMAN
5	770	100.0	208	2	Q8NF19 HUMAN
6	770	100.0	215	1	Q8NF19 RAT
7	754.5	98.0	213	2	Q8NF19 SHEEP
8	748.5	97.2	213	2	Q8NF19 SHEEP
9	734	95.3	209	1	Q8NF19 MOUSE
10	734	95.3	209	2	Q8NF19 MOUSE
11	707	91.8	209	2	Q8NF19 MOUSE
12	686	89.1	212	2	Q8NF19 CHICK
13	597.5	77.6	154	2	Q8NF19 BOVIN
14	565	73.4	201	2	Q8NF19 AMBME
15	521	67.7	149	2	Q8NF19 TETNG
16	498	64.7	201	2	Q8NF19 BRARE
17	497	64.5	111	2	Q8NF19 XENLA
18	497	64.5	201	2	Q8NF19 BRARE
19	488	63.4	134	2	Q8NF19 AMBME
20	480	62.3	112	2	Q8NF19 AMBME
21	479	62.2	191	2	Q8NF19 BRARE
22	437	56.8	162	2	Q8NF19 RAT
23	435	56.5	162	1	Q8NF19 MOUSE
24	434.5	56.3	194	1	Q8NF19 SHEEP
25	433.5	56.3	194	1	Q8NF19 CANFA
26	432.5	56.2	194	1	Q8NF19 CEREL
27	432.5	56.2	194	1	Q8NF19 HUMAN
28	432.5	56.2	194	2	Q8NF19 HUMAN
29	432.5	56.2	194	2	Q8NF19 HUMAN
30	432	56.1	170	1	Q8NF19 HUMAN
31	429.5	55.8	194	1	Q8NF19 MOUSE

32	429.5	55.8	194	2	Q8NF19 MOUSE	Q544i6 mus musculus
33	428.5	55.6	194	2	Q8NF19 CHICK	Q5kra4 gallus gall
34	428.5	55.0	194	1	Q8NF19 PIG	Q9n198 sus scrofa
35	420.5	54.6	194	2	Q8NF19 XENTR	Q5m7n7 xenopus tro
36	416.5	54.1	194	1	Q8NF19 RAT	Q02195 rattus norv
37	414.5	53.8	194	2	Q8NF19 XENLA	Q4k195 xenopus lae
38	413.5	53.7	194	2	Q8NF19 XENLA	Q8c386 mus musculus
39	396.5	51.5	186	2	Q8NF19 MUSVI	Q95147 mustela vis
40	391.5	50.8	185	2	Q8NF19 RAT	Q9ern5 rattus norv
41	369	47.9	256	1	Q8NF19 BRARE	P48802 brachydanio
42	363	47.1	220	1	Q8NF19 CHICK	P48801 gallus gall
43	358	46.5	236	2	Q8NF19 XENTR	Q661f7 xenopus tro
44	358	46.5	237	1	Q8NF19 XENLA	P36386 xenopus lae
45	353.5	45.9	245	2	Q8NF19 RAT	Q8r519 rattus norv

ALIGNMENTS

RESULT 1

Q8NF19 HUMAN PRELIMINARY; PRT; 170 AA.
 AC Q8NF19;
 DT 01-OCT-2002 (Tremblrel. 22, Created)
 DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
 DE Fibroblast growth factor 10 (fragment).
 GN Name=FGF10;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RC NUCLEOTIDE SEQUENCE.
 RP TISSUE=Bladder;
 RX MEDLINE=22075097; PubMed=11923311; DOI=10.1074/jbc.M201658200;
 RA Bagai S., Rubio E., Cheng J.F., Sweet R., Thomas R., Fuchs E.,
 RA Grady R., Mitchell M., Baesuk J.A.;
 RT "Fibroblast growth factor-10 is a mitogen for urothelial cells.";
 J. Biol. Chem. 277:23828-23837(2002).
 DR EMBL; AF508782; AAM46926.1; -, mRNA.
 DR HSSP; O15520; 1NUN.
 DR GO; GO:0008083; F: growth factor activity; IEA.
 DR InterPro; IPR002209; HB/P: growth factor.
 DR InterPro; IPR002348; IL1_HBGF.
 DR Pfam; PF00167; FGF; 1.
 DR PRINTS; PR00263; HBGF; 1.
 DR PRINTS; PR00262; IL1_HBGF.
 DR PRODOM; PD000831; IL1_HBGF; 1.
 DR SMART; SM00442; FGF; 1.
 DR PROSITE; PS00247; HBGF_FGF; 1.
 DR Growth factor.
 FT NON TER 1
 SQ SEQUENCE 170 AA; 19195 MW; 4EA43515F758327A CRC64;

Query Match 100.0%; Score 770; DB 2; Length 170;
 Best Local Similarity 100.0%; Pred. No. 2.6e-65;
 Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	RHVSYNHLQGDVWRKLFSTTKYFLKIKNGKVGSGTKKNCPCYSILEITSVEIGVAVK 60
Db	27	RHVSYNHLQGDVWRKLFSTTKYFLKIKNGKVGSGTKKNCPCYSILEITSVEIGVAVK 86
Qy	61	AINSNYLANMKKGLYSGSEFNNDCKLKERIENGNTYASFNWQNGRQMYVALNGK 120
Db	87	AINSNYLANMKKGLYSGSEFNNDCKLKERIENGNTYASFNWQNGRQMYVALNGK 146
Qy	121	APRRGQTRKNTSAHFLPMVHS 144
Db	147	APRRGQTRKNTSAHFLPMVHS 170

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OM protein - protein search, using sw model

Run on: April 3, 2006, 06:52:49 ; Search time 65 Seconds
(without alignments)
925.653 Million cell updates/sec

Title: US-10-665-526-2_COPY_65_208

Perfect score: 770

Sequence: 1 RHVRSYNHLQGVWRKLFs.....GQTRKRKNTSAHFLPMVHS 144

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 101

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%

Maximum Match 100%

Listing first 750 summaries

Database : Published Applications AA Main.*

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*

2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*

3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*

4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*

5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*

6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	770	100.0	147	3	US-09-345-373-68
2	770	100.0	147	4	US-10-194-443-4
3	770	100.0	147	4	US-10-075-446-68
4	770	100.0	147	4	US-10-035-212-68
5	770	100.0	147	5	US-10-733-311-68
6	770	100.0	147	5	US-10-901-210-68
7	770	100.0	152	4	US-10-665-526-6
8	770	100.0	170	4	US-10-314-372-6
9	770	100.0	171	3	US-09-345-373-116
10	770	100.0	171	4	US-10-075-446-116
11	770	100.0	171	4	US-10-035-212-116
12	770	100.0	171	5	US-10-733-311-116
13	770	100.0	171	5	US-10-901-210-116
14	770	100.0	174	3	US-09-345-373-43
15	770	100.0	174	3	US-09-345-373-55
16	770	100.0	174	3	US-09-345-373-66
17	770	100.0	174	4	US-10-194-443-10
18	770	100.0	174	4	US-10-194-443-12
19	770	100.0	174	4	US-10-075-446-43
20	770	100.0	174	4	US-10-075-446-65
21	770	100.0	174	4	US-10-075-446-66
22	770	100.0	174	4	US-10-035-212-43
23	770	100.0	174	4	US-10-035-212-55
24	770	100.0	174	4	US-10-035-212-66
25	770	100.0	174	5	US-10-733-311-43
26	770	100.0	174	5	US-10-733-311-55
27	770	100.0	174	5	US-10-733-311-66

28	770	100.0	174	5	US-10-901-210-43	Sequence 43, Appl
29	770	100.0	174	5	US-10-901-210-55	Sequence 55, Appl
30	770	100.0	174	5	US-10-901-210-66	Sequence 66, Appl
31	770	100.0	184	3	US-09-345-373-30	Sequence 30, Appl
32	770	100.0	184	4	US-10-075-446-30	Sequence 30, Appl
33	770	100.0	184	4	US-10-035-212-30	Sequence 30, Appl
34	770	100.0	184	5	US-10-733-311-30	Sequence 30, Appl
35	770	100.0	184	5	US-10-901-210-30	Sequence 30, Appl
36	770	100.0	195	4	US-10-314-372-4	Sequence 4, Appl
37	770	100.0	208	3	US-09-822-485-13	Sequence 13, Appl
38	770	100.0	208	3	US-09-853-666-2	Sequence 2, Appl
39	770	100.0	208	3	US-09-750-963-4	Sequence 4, Appl
40	770	100.0	208	3	US-09-425-021-20	Sequence 20, Appl
41	770	100.0	208	3	US-09-345-373-2	Sequence 2, Appl
42	770	100.0	208	3	US-09-345-373-20	Sequence 20, Appl
43	770	100.0	208	3	US-09-345-373-24	Sequence 24, Appl
44	770	100.0	208	3	US-09-345-373-39	Sequence 39, Appl
45	770	100.0	208	4	US-10-081-347-30	Sequence 30, Appl
46	770	100.0	208	4	US-10-194-443-2	Sequence 2, Appl
47	770	100.0	208	4	US-10-194-443-8	Sequence 8, Appl
48	770	100.0	208	4	US-10-075-446-2	Sequence 2, Appl
49	770	100.0	208	4	US-10-075-446-20	Sequence 20, Appl
50	770	100.0	208	4	US-10-075-446-24	Sequence 24, Appl
51	770	100.0	208	4	US-10-075-446-39	Sequence 39, Appl
52	770	100.0	208	4	US-10-314-372-2	Sequence 2, Appl
53	770	100.0	208	4	US-10-374-207-13	Sequence 13, Appl
54	770	100.0	208	4	US-10-035-212-2	Sequence 2, Appl
55	770	100.0	208	4	US-10-035-212-20	Sequence 20, Appl
56	770	100.0	208	4	US-10-035-212-24	Sequence 24, Appl
57	770	100.0	208	4	US-10-035-212-39	Sequence 39, Appl
58	770	100.0	208	4	US-10-131-985-11	Sequence 11, Appl
59	770	100.0	208	4	US-10-315-431-30	Sequence 30, Appl
60	770	100.0	208	4	US-10-665-526-2	Sequence 2, Appl
61	770	100.0	208	4	US-10-695-957-2	Sequence 2, Appl
62	770	100.0	208	4	US-10-302-812-36	Sequence 36, Appl
63	770	100.0	208	4	US-10-037-922-30	Sequence 30, Appl
64	770	100.0	208	4	US-10-322-696-48	Sequence 48, Appl
65	770	100.0	208	4	US-10-727-195-24	Sequence 24, Appl
66	770	100.0	208	5	US-10-733-311-2	Sequence 2, Appl
67	770	100.0	208	5	US-10-733-311-20	Sequence 20, Appl
68	770	100.0	208	5	US-10-733-311-24	Sequence 24, Appl
69	770	100.0	208	5	US-10-733-311-39	Sequence 39, Appl
70	770	100.0	208	5	US-10-901-210-11	Sequence 11, Appl
71	770	100.0	208	5	US-10-868-577A-50	Sequence 50, Appl
72	770	100.0	208	5	US-10-901-210-2	Sequence 2, Appl
73	770	100.0	208	5	US-10-901-210-20	Sequence 20, Appl
74	770	100.0	208	5	US-10-901-210-24	Sequence 24, Appl
75	770	100.0	208	5	US-10-901-210-39	Sequence 39, Appl
76	770	100.0	208	5	US-10-854-485-30	Sequence 30, Appl
77	770	100.0	208	5	US-10-756-149-5464	Sequence 5464, Ap
78	770	100.0	208	5	US-10-775-204-468	Sequence 468, App
79	770	100.0	208	5	US-10-775-204-469	Sequence 469, App
80	770	100.0	208	5	US-10-775-204-497	Sequence 497, App
81	770	100.0	208	5	US-10-775-204-498	Sequence 498, App
82	770	100.0	208	5	US-10-775-204-645	Sequence 645, App
83	770	100.0	208	5	US-10-775-204-646	Sequence 646, App
84	770	100.0	208	5	US-10-775-204-1684	Sequence 1684, Ap
85	770	100.0	208	5	US-10-775-204-1685	Sequence 1685, Ap
86	770	100.0	208	5	US-10-775-204-1692	Sequence 1692, Ap
87	770	100.0	208	5	US-10-775-204-1693	Sequence 1693, Ap
88	770	100.0	208	5	US-10-775-204-1694	Sequence 1694, Ap
89	770	100.0	208	5	US-10-775-204-1698	Sequence 1698, Ap
90	770	100.0	208	5	US-09-925-302-586	Sequence 586, App
91	770	100.0	243	3	US-09-925-302-586	Sequence 586, App
92	770	100.0	243	3	US-10-775-204-1524	Sequence 1524, Ap
93	770	100.0	749	5	US-10-775-204-1525	Sequence 1525, Ap
94	770	100.0	749	5	US-10-775-204-1526	Sequence 1526, Ap
95	770	100.0	749	5	US-10-775-204-1520	Sequence 1520, Ap
96	770	100.0	755	5	US-10-775-204-252	Sequence 252, App
97	770	100.0	755	5	US-10-775-204-253	Sequence 253, App
98	770	100.0	755	5	US-10-775-204-281	Sequence 281, App
99	770	100.0	755	5	US-10-775-204-282	Sequence 282, App
100	770	100.0	755	5	US-10-775-204-282	Sequence 282, App

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OM protein - protein search, using sw model

Run on: April 3, 2006, 06:46:39 ; Search time 189 Seconds
(without alignment)
334.765 Million cell updates/sec

Title: US-10-665-526-2_COPY_65_208
Perfect score: 770
Sequence: 1 RHVSYNHLQGVWRKLES.....GQTRKNTSAFLPMVHVS 144

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 133

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 100%
Maximum Match 100%
Listing first 750 summaries

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- 2: Geneseq1990s.*
- 3: Geneseq2000s.*
- 4: Geneseq2001s.*
- 5: Geneseq2002s.*
- 6: Geneseq2003as.*
- 7: Geneseq2003bs.*
- 8: Geneseq2004s.*
- 9: Geneseq2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	770	100.0	146	2	AAW52584 KGF-2 del
2	770	100.0	146	4	AAW60204 Mutant hu
3	770	100.0	147	2	AAW32899 E. coli o
4	770	100.0	147	3	AAW10314 Human KGF
5	770	100.0	147	4	AAW61678 KGF-2 del
6	770	100.0	147	6	ABP71397 KGF-2 tru
7	770	100.0	147	6	ABP54294 KGF-2 del
8	770	100.0	147	6	ADA95504 Human ker
9	770	100.0	147	7	ADD66177 Human KGF
10	770	100.0	147	8	ADT97975 Human KGF
11	770	100.0	152	2	AAW57312 Human KGF
12	770	100.0	162	2	AAW52583 KGF-2 del
13	770	100.0	162	4	AAW60207 Human KGF
14	770	100.0	170	2	AAW52582 KGF-2 del
15	770	100.0	170	2	AAW59054 Human hfg
16	770	100.0	170	4	AAW60206 Human KGF
17	770	100.0	170	8	ADU48553 Murine KG
18	770	100.0	171	2	AAW53798 KGF-2 mut
19	770	100.0	171	2	AAW32908 E. coli op
20	770	100.0	171	3	AAW10324 Human KGF
21	770	100.0	171	4	AAW61688 KGF-2 mut
22	770	100.0	171	6	ABP54304 KGF-2 del
23	770	100.0	171	6	ADA95552 E. coli k
24	770	100.0	171	7	ADD66225 Human KGF

25	770	100.0	171	7	ADO17773 Keratinoc
26	770	100.0	171	8	ADT98023 Human KGF
27	770	100.0	174	2	AAW53793 E. coli op
28	770	100.0	174	2	AAW32897 E. coli o
29	770	100.0	174	2	AAW32896 Truncated
30	770	100.0	174	2	AAW32898 E. coli o
31	770	100.0	174	3	AAW10311 Human KGF
32	770	100.0	174	3	AAW10312 Human KGF
33	770	100.0	174	3	AAW10313 Human KGF
34	770	100.0	174	4	AAW61676 Escherich
35	770	100.0	174	4	AAW61677 KGF-2 del
36	770	100.0	174	4	AAW61675 Escherich
37	770	100.0	174	6	ABP71401 Alternate
38	770	100.0	174	6	ABP71400 E. coli o
39	770	100.0	174	6	ABP54293 KGF-2 del
40	770	100.0	174	6	ABP54291 E. coli o
41	770	100.0	174	6	ABP54292 E. coli o
42	770	100.0	174	6	ADA95491 E. coli k
43	770	100.0	174	6	ADA95479 E. coli k
44	770	100.0	174	6	ADA95502 Human ker
45	770	100.0	174	7	ADD66175 Human KGF
46	770	100.0	174	7	ADD66152 E. coli o
47	770	100.0	174	7	ADD66164 E. coli o
48	770	100.0	174	8	ADT97950 Human ker
49	770	100.0	174	8	ADT97962 Human ker
50	770	100.0	174	8	ADT97973 Human KGF
51	770	100.0	184	2	AAW32917 E. coli op
52	770	100.0	184	2	AAW10309 Human KGF
53	770	100.0	184	4	AAW61673 PQE60-Cyb
54	770	100.0	184	6	ABP54289 pQE60-Cyb
55	770	100.0	184	6	ADA95466 Synthetic
56	770	100.0	184	7	ADD66139 Human mat
57	770	100.0	184	8	ADT97937 Human ker
58	770	100.0	195	2	AAW59053 His rFGF1
59	770	100.0	206	4	AAW60213 Human KGF
60	770	100.0	208	2	AAW24050 Human fib
61	770	100.0	208	2	AAW53792 E. coli op
62	770	100.0	208	2	AAW52581 Keratinoc
63	770	100.0	208	2	AAW57264 Recombina
64	770	100.0	208	2	AAW59052 Human ker
65	770	100.0	208	2	AAW92312 Human FGF
66	770	100.0	208	2	AAW89412 Human fib
67	770	100.0	208	2	AAW84564 Human fib
68	770	100.0	208	2	AAW32888 Human ker
69	770	100.0	208	2	AAW32916 Human ker
70	770	100.0	208	2	AAW32895 E. coli o
71	770	100.0	208	3	AAW70688 Human fib
72	770	100.0	208	3	AAW10310 Human KGF
73	770	100.0	208	3	AAW10304 Human ker
74	770	100.0	208	3	AAW10301 Fibroblas
75	770	100.0	208	3	AAW10293 Human ker
76	770	100.0	208	4	AAW84600 Amino aci
77	770	100.0	208	4	AAW61674 Escherich
78	770	100.0	208	4	AAW61657 Human ker
79	770	100.0	208	4	AAW60201 Human ker
80	770	100.0	208	4	AAW5821 Human myo
81	770	100.0	208	4	AAW5821 Human fib
82	770	100.0	208	5	AAW18815 Human FGF
83	770	100.0	208	5	AAW99131 Human fib
84	770	100.0	208	6	AAW19673 Human KGF
85	770	100.0	208	6	ABP71396 Keratinoc
86	770	100.0	208	6	ABP71399 E. coli o
87	770	100.0	208	6	ABP54281 Human ker
88	770	100.0	208	6	ABP54284 Human ker
89	770	100.0	208	6	ABP54273 Human ker
90	770	100.0	208	6	ABP54290 E. coli k
91	770	100.0	208	6	ADA95460 Human ker
92	770	100.0	208	6	ADA95456 Fibroblas
93	770	100.0	208	6	ADA95475 E. coli k
94	770	100.0	208	7	ADD66133 Human ful
95	770	100.0	208	7	ADD66111 Human ker
96	770	100.0	208	7	ADD66129 Human ker
97	770	100.0	208	7	ADD66129 Human ker

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OM protein - protein search, using sw model
Run on: April 3, 2006, 06:49:28 ; Search time 46 Seconds
(without alignments)
258.811 Million cell updates/sec
Title: US-10-665-526-2_COPY_65_208
Perfect score: 770
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 572060 seqs, 82675679 residues
Total number of hits satisfying chosen parameters: 63
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 100%
Maximum Match 100%
Listing first 750 summaries
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3: /cgn2_6/prodata/1/iaa/H COMB.pep.*
4: /cgn2_6/prodata/1/iaa/PCTUS COMB.pep.*
5: /cgn2_6/prodata/1/iaa/RE COMB.pep.*
6: /cgn2_6/prodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	770	100.0	147	2	US-09-023-082A-68
2	770	100.0	147	2	US-09-248-998-68
3	770	100.0	147	2	US-09-610-651-68
4	770	100.0	147	2	US-09-345-373-68
5	770	100.0	147	2	US-10-075-446-68
6	770	100.0	152	2	US-09-284-100A-6
7	770	100.0	171	2	US-09-023-082A-116
8	770	100.0	171	2	US-09-248-998-116
9	770	100.0	171	2	US-09-610-651-116
10	770	100.0	171	2	US-09-345-373-116
11	770	100.0	171	2	US-10-075-446-116
12	770	100.0	174	2	US-09-023-082A-43
13	770	100.0	174	2	US-09-023-082A-55
14	770	100.0	174	2	US-09-023-082A-66
15	770	100.0	174	2	US-09-248-998-43
16	770	100.0	174	2	US-09-248-998-55
17	770	100.0	174	2	US-09-248-998-66
18	770	100.0	174	2	US-09-610-651-43
19	770	100.0	174	2	US-09-610-651-55
20	770	100.0	174	2	US-09-610-651-66
21	770	100.0	174	2	US-09-345-373-43
22	770	100.0	174	2	US-09-345-373-55
23	770	100.0	174	2	US-09-345-373-66
24	770	100.0	174	2	US-10-075-446-43
25	770	100.0	174	2	US-10-075-446-55
26	770	100.0	174	2	US-10-075-446-66
27	770	100.0	184	2	US-09-023-082A-30

28	770	100.0	184	2	US-09-248-998-30	Sequence 30, Appl
29	770	100.0	184	2	US-09-610-651-30	Sequence 30, Appl
30	770	100.0	184	2	US-09-345-373-30	Sequence 30, Appl
31	770	100.0	184	2	US-10-075-446-30	Sequence 30, Appl
32	770	100.0	208	1	US-08-462-169B-20	Sequence 20, Appl
33	770	100.0	208	1	US-08-951-822-30	Sequence 30, Appl
34	770	100.0	208	2	US-09-103-079-20	Sequence 20, Appl
35	770	100.0	208	2	US-09-023-082A-2	Sequence 2, Appl
36	770	100.0	208	2	US-09-023-082A-20	Sequence 20, Appl
37	770	100.0	208	2	US-09-023-082A-24	Sequence 24, Appl
38	770	100.0	208	2	US-09-023-082A-39	Sequence 39, Appl
39	770	100.0	208	2	US-09-218-444-2	Sequence 2, Appl
40	770	100.0	208	2	US-09-368-951-30	Sequence 30, Appl
41	770	100.0	208	2	US-09-425-021-20	Sequence 20, Appl
42	770	100.0	208	2	US-09-229-947-30	Sequence 30, Appl
43	770	100.0	208	2	US-09-564-829-14	Sequence 14, Appl
44	770	100.0	208	2	US-09-248-998-2	Sequence 2, Appl
45	770	100.0	208	2	US-09-248-998-20	Sequence 20, Appl
46	770	100.0	208	2	US-09-248-998-24	Sequence 24, Appl
47	770	100.0	208	2	US-09-248-998-39	Sequence 39, Appl
48	770	100.0	208	2	US-09-853-666-2	Sequence 2, Appl
49	770	100.0	208	2	US-09-610-651-2	Sequence 2, Appl
50	770	100.0	208	2	US-09-610-651-20	Sequence 20, Appl
51	770	100.0	208	2	US-09-610-651-24	Sequence 24, Appl
52	770	100.0	208	2	US-09-610-651-39	Sequence 39, Appl
53	770	100.0	208	2	US-09-284-100A-2	Sequence 2, Appl
54	770	100.0	208	2	US-09-949-016-8982	Sequence 8982, Ap
55	770	100.0	208	2	US-09-585-541-2	Sequence 2, Appl
56	770	100.0	208	2	US-09-345-373-2	Sequence 2, Appl
57	770	100.0	208	2	US-09-345-373-20	Sequence 20, Appl
58	770	100.0	208	2	US-09-345-373-24	Sequence 24, Appl
59	770	100.0	208	2	US-09-345-373-39	Sequence 39, Appl
60	770	100.0	208	2	US-10-075-446-2	Sequence 2, Appl
61	770	100.0	208	2	US-10-075-446-20	Sequence 20, Appl
62	770	100.0	208	2	US-10-075-446-24	Sequence 24, Appl
63	770	100.0	208	2	US-10-075-446-39	Sequence 39, Appl

ALIGNMENTS

RESULT 1
US-09-023-082A-68
; Sequence 68, Application US/09023082A
; Patent No. 6077692
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; APPLICANT: GENTZ, REINER L.
; TITLE OF INVENTION: KERATINOCYTE GROWTH FACTOR-2
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; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

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